has a spectrum with broad peaks and no dispersion, which is indicative of a collapsed but disordered and fluctuating structure or non-specific association. All seven mutant proteins retain their ability to bind 1gG as measured by binding to an 1gG-Sepharose affinity column. The stability and native-like character of $\Delta h_{\alpha\beta}[-1.50\mbox{\normalfont A}]$ and $\Delta h_{1\beta}[+1.50\mbox{\normalfont A}]$ indicate that the sequence selection algorithm is sufficiently robust to tolerate Δh perturbations that are as large as 15% of GB1's native height super-secondary structure parameter value of 10 Å.--

In the Claims:

Please cancel claim 1 without prejudice or disclaimer.

Please add the following claims:

- --30. A computer readable memory that upon execution by a computer processor carries out the following functions:
 - a) alters at least one supersecondary structure parameter value of a protein backbone structure;
 - b) correlates a group of potential rotamers for residue positions of said protein backbone structure; and
 - c) analyzes the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences.
 - 31. A computer readable memory according to claim 30 wherein said ranking module includes a van der Waals scoring function component.